Homologous Recombination Deficiency (HRD) Score Predicts Response to Platinum-Containing Neoadjuvant Chemotherapy in Patients with Triple-Negative Breast Cancer


Abstract

Purpose: BRCA1/2-mutated and some sporadic triple-negative breast cancers (TNBC) have DNA repair defects and are sensitive to DNA-damaging therapeutics. Recently, three independent DNA-based measures of genomic instability were developed on the basis of loss of heterozygosity (LOH), telomeric allelic imbalance (TAI), and large-scale state transitions (LST).

Experimental Design: We assessed a combined homologous recombination deficiency (HRD) score, an unweighted sum of LOH, TAI, and LST scores, in three neoadjuvant TNBC trials of platinum-containing therapy. We then tested the association of HRD deficiency, defined as HRD score $\geq 42$ or BRCA1/2 mutation, with response to platinum-based therapy.

Results: In a trial of neoadjuvant platinum, gemcitabine, and iniparib, HR deficiency predicted residual cancer burden score of 0 or 1 (RCB 0/I) and pathologic complete response (pCR; OR = 4.96, P = 0.0036; OR = 6.52, P = 0.0058). HR deficiency remained a significant predictor of RCB 0/I when adjusted for clinical variables (OR = 5.86, P = 0.012). In two other trials of neoadjuvant cisplatin therapy, HR deficiency predicted RCB 0/I and pCR (OR = 10.18, P = 0.0011; OR = 17.00, P = 0.0066). In a multivariable model of RCB 0/I, HR deficiency retained significance when clinical variables were included (OR = 12.08, P = 0.0017). When restricted to BRCA1/2 nonmutated tumors, response was higher in patients with high HRD scores: RCB 0/I P = 0.062, pCR P = 0.063 in the neoadjuvant platinum, gemcitabine, and iniparib trial; RCB 0/I P = 0.039, pCR P = 0.018 in the neoadjuvant cisplatin trials.

Conclusions: HR deficiency identifies TNBC tumors, including BRCA1/2 nonmutated tumors more likely to respond to platinum-containing therapy. Clin Cancer Res 1-10. ©2016 AACR.

Introduction

Triple-negative breast cancers (TNBC) lack expression of estrogen and progesterone receptors and overexpression or amplification of the HER2/neu oncogene, and are therefore not amenable to therapy directed at these targets. Sporadic (BRCA1 and BRCA2 germline wild-type) TNBCs share many characteristics with BRCA1 mutation–associated cancers, including a basal-like gene expression profile, frequent p53 mutations, and a high burden of genomic aberrations such as loss of heterozygosity (1–7). BRCA1 or BRCA2 (BRCA1/2)-mutated cancers have defects in several aspects of DNA repair including homologous recombination deficiency (HRD; refs. 1, 8). BRCA1/2 mutation–associated cancers have been shown to have increased sensitivity to DNA cross-linking agents such as platinum salts (9). A number of studies have suggested that some sporadic TNBC may bear substantial similarities to BRCA1/2-mutated cancers, including harboring DNA repair defects that might predispose to platinum sensitivity (1, 10, 11). Confirming this concept, two neoadjuvant clinical trials have demonstrated that a subset of sporadic, non-BRCA1/2–mutated TNBC are sensitive to single-agent platinum chemotherapy (12, 13). Furthermore, several recent randomized trials have shown improvement in pathologic response with the addition of platinum to standard-of-care neoadjuvant regimens for TNBC but at the cost of increased toxicity (14–16). A predictive biomarker for platinum sensitivity would be helpful to personalize the use of platinum agents, restricting their use to those who would benefit while avoiding unnecessary toxicity for those who would not.
Recently, three independent DNA-based measures of genomic instability reflecting underlying tumor homologous recombination DNA repair deficiency have been developed on the basis of loss of heterozygosity (LOH; ref. 17), telomeric allelic imbalance (TAI; ref. 18), and large-scale state transitions (LST; ref. 19). Although each individual metric is significantly associated with BRCA1/2 status, the combination of the three scores performed best at distinguishing homologous recombination deficient from nondeficient tumors (20, 21). We have previously shown that the homologous recombination deficiency loss of heterozygosity (HRD-LOH) score is significantly associated with favorable response to neoadjuvant platinum-based therapy in a phase II trial of gemcitabine, carboplatin, and iniparib (PrECOG 0105; ref. 22). In addition, in a pooled analysis of two other platinum-based neoadjuvant studies, we showed that the number of regions of TAI, predicted for favorable pathologic response in TNBC, and was also associated with platinum sensitivity in ovarian cancer (18).

In this study, we set out to evaluate the combined homologous recombination deficiency score (HRD score), defined as the unweighted numeric sum of LOH, TAI, and LST and test the predictive power of the HRD score threshold. The HRD score threshold was predefined by analyzing HRD scores in a training cohort of 497 breast and 561 ovarian chemotherapynaive tumors with known BRCA1/2 status, and identifying a cutoff with 95% sensitivity to detect those tumors with BRCA1/2 mutations or BRCA1 promoter methylation. HR deficiency, defined as HRD score ≥42 and/or tumor BRCA1/2 mutation, was tested for its ability to identify which tumors responded to neoadjuvant platinum-containing chemotherapy in patients with TNBC.

The PrECOG 0105 study included 93 stage I–IIIA (T ≥ 1 cm) triple-negative and/or BRCA1/2 mutation-associated breast cancer patients, treated with either 4 or 6 cycles of carboplatin, gemcitabine, and iniparib in the neoadjuvant setting. The two cisplatin neoadjuvant studies (Cisplatin-1 and Cisplatin-2) enrolled 79 TNBC patients with stage II or III disease. Cisplatin-1 utilized 4 cycles of cisplatin monotherapy in 28 patients (12), whereas Cisplatin-2 added bevacizumab to the same cisplatin backbone in 51 patients (13). As the response rates for the Cisplatin-1 and Cisplatin-2 trials were similar, these trials were pooled for further analysis. In the current study, the PrECOG 0105 cohort and the pooled Cisplatin-1 and Cisplatin-2 trials were analyzed to determine the association of HR deficiency with pathologic response.
been validated as an independent prognostic marker of distant relapse-free survival in patients with breast cancer treated with neoadjuvant chemotherapy (RCB 0, complete pathologic response; RCB I, minimal residual disease; RCB II, moderate residual disease; and RCB III, extensive residual disease). For this analysis, two dichotomous measures of tumor response were used, RCB 0/1 yes versus no and pathologic complete response (pCR) yes versus no. pCR was defined as RCB score 0 and requires no residual invasive or metastatic carcinoma in breast or lymph nodes. “RCB 0/1 yes” includes pathologic response classes of pCR or RCB-I; “RCB 0/1 no” includes pathologic responses classes RCB-II or RCB-III.

Tissue processing
For each patient sample, five to ten 5-μm tissue sections from a pretreatment tumor core biopsy were sent to Myriad Genetics, Inc. and processed in the research laboratory according to the CLIA protocol. DNA extraction from formalin-fixed paraffin-embedded (FFPE) or frozen tumors is described in the Supplementary Materials. For PrECOG 0105, 3 samples could not be processed due to insufficient tumor tissue, leaving 90 sufficient for processing. For the two neoadjuvant cisplatin clinical trials, 17 of 79 patient samples had exhausted tumor blocks or insufficient tumor tissue, thus DNA was extracted from 62 samples.

Molecular analyses
DNA was analyzed using the recently described next-generation sequencing–based assay to generate genome-wide SNP profiles from which the three components of the HRD score are calculated (20). A custom enrichment panel was developed, which targets 54,091 single-nucleotide polymorphisms (SNP) distributed across the complete human genome. The panel also includes an additional 685 probes targeting the complete coding region of BRCA1 and BRCA2. A detailed description of the panel design and development and the assay process is provided in Timms and colleagues (20).

MIP SNP arrays have been previously described in detail (27). For PrECOG 0105, MIP SNP array data had previously been generated on 55 samples from this study. In 31 samples with HRD scores from both arrays and sequencing, the Pearson correlation was 0.94. The sequencing-based HRD assay was used for molecular data for 60 of the 70 samples in the analysis set and a whole genome MIP array was used to generate data for the remaining 10 where sequencing data were not available (3 with insufficient tissue and 7 where sequencing failed). The sequencing-based HRD assay was used for all of the cisplatin trial cohort samples.

To determine BRCA1/2 mutation status, variant and large rearrangement detection was performed on sequence from BRCA1 and BRCA2. Complete descriptions of the sequence alignment and mutation detection methods are provided in Timms and colleagues (20). Mutations identified were only included in the analysis if classified as deleterious or suspected deleterious based on previously described criteria (28).

To calculate the HRD score for samples analyzed by custom hybridization sequencing assay, reads covering SNP positions were used to generate allelic imbalance profiles as described by Timms and colleagues (20). HRD score was defined as the unweighted sum of LOH, TAI, and LST scores: HRD = LOH + TAI + LST. Details of the individual LOH, TAI, and LST scores, as well as the combined HRD score, are described in the Supplementary Material.

HR deficiency status was determined on the basis of the combination of the dichotomized HRD score using the predefined HRD threshold and tumor BRCA1/2 status (scored as mutated if deleterious or suspected deleterious mutations in BRCA1/2 were present; nonmutated if otherwise, including variants of uncertain significance). HR deficiency was defined as high HRD score (above the HRD threshold, ≥ 42) and/or mutated tumor BRCA1/2. HR nondeficiency was defined as low HRD score (below the HRD threshold, <42) and nonmutated or failed tumor BRCA1/2 mutation analysis. HR status could not be determined if HRD score analysis failed and tumor BRCA1/2 analysis was negative or failed.

Analysis cohorts
The PrECOG 0105 trial cohort consisted of 93 patients. Excluding those with insufficient tumor for processing and/or who did not complete at least four cycles of treatment left 86 samples. Eighty-three of 86 (97%) samples generated tumor BRCA1/2 mutation data, and HR score analysis was successful for 68 of 86 (79%) tumors, which provided 70 of 86 (81%) samples with HR deficiency status and clinical response data for statistical analysis. Of the 90 tumors submitted for molecular assay, 52 were HR deficient including one missing response (58%), 21 were HR nondeficient (23%), and 17 were undetermined (19%; Supplementary Fig. S1A).

The combined cisplatin trials cohort consisted of 79 patients, of which 17 had insufficient tumor for processing. Fifty-three of 62 (85%) passed BRCA1/2 mutation screening, HRD score analysis was successful for 51 of 62 (82%), and HR deficiency status was determined for 53 of 62 (85%). Of the 62 tumors subjected to molecular assay, 31 were HR deficient including 2 missing response (50%), 22 were nondeficient including 1 missing response (35%), and 9 were undetermined (15%; Supplementary Fig. S1B). After removing the three samples with missing response data, there were 50 samples evaluable for statistical analysis of HR deficiency and response. The combined cisplatin cohort was not used in the development of the HRD score, HRD threshold, or any of the individual components of the HRD score (LOH, TAI, LST), but were the first two cohorts in which TAI was tested. As such, this cohort offers an independent test of the HRD score threshold and the HR deficiency predictor.

Statistical analysis
For the PrECOG 0105 cohort, statistical analysis was performed on the set of 70 samples with HR deficiency status and response or on nested subsets (68 had HRD scores; 68 had BRCA1/2 mutation screening of which 22/68 had BRCA1/2 mutations identified; 66 had HRD scores and BRCA1/2 mutation screening of which 46/66 were BRCA1/2 wild-type). For the cisplatin trials cohort, analysis was performed on the set of 50 samples with HR deficiency status and response, or on nested subsets (48 had HRD scores; 47 had BRCA1/2 mutation screening of which 9/47 had BRCA1/2 mutations identified; 45 had HRD scores and BRCA1/2 mutation screening of which 38/45 were BRCA1/2 wild-type).

Statistical analysis for both cohorts was conducted according to the statistical analysis plan that was prespecified for the cisplatin trials cohort. The primary endpoint was RCB 0/1 with a secondary endpoint of pCR. The primary objective was to test the association of HR deficiency. The secondary objectives were to test
individually the association of quantitative HRD score and tumor BRCA1/2 status with RCB 0/I. A subgroup analysis of dichotomous HRD score was conducted in BRCA1/2 wild-type. Each analysis was then repeated with the secondary endpoint of pCR.

Logistic regression was used to test association with binary response in univariate and multivariable models, and to test association of clinical variables and HRD score with BRCA1/2 mutation. We report the OR for the interquartile range (IQR) of numerical variables, or for each category relative to the reference, with a 95% confidence interval. The \( P \) value for each covariate was calculated from the change in the likelihood deviance between the full and an appropriate reduced model, with and without the covariate of interest.

HR deficiency was modeled as a predictor of response with logistic regression methods. Standard maximum likelihood statistics were used to test RCB 0/I; Firth’s penalized likelihood was used to adjust for small sample bias and produce confidence intervals in models of pCR with no events in the HR nondeficient category.

Statistical inference was conducted within the R software environment (29). Statistical significance was set at the 5% level. All \( P \) values and confidence intervals are two-sided with no adjustment for multiple testing.

Results

Establishing a threshold for the combined HRD score

The training set to determine a threshold for the combined HRD score was assembled from 4 cohorts [497 breast and 561 ovarian cases (20, 23–25)], and included 78 breast and 190 ovarian tumors with BRCA1/2 deficiency based on tumor mutation screening and promoter methylation analysis. These four cohorts used for training the HRD threshold are completely independent from and have no overlap with PrECOG 0105 and the cisplatin cohorts analyzed below. The distribution of HRD scores in the training set is shown in Fig. 1 and has an apparent bimodal distribution with a nadir between 40 and 45. The HRD threshold was selected to have a high sensitivity for detecting HR deficiency in breast and ovarian cancer. It was assumed that the loss of BRCA1/2 function results in HR deficiency, and that the distribution of HRD scores in BRCA1/2-deficient samples would represent the distribution of scores in HR-deficient samples due to any underlying mechanism. To obtain a sensitivity of at least 95%, the threshold was set at the 5th percentile of the HRD scores in this training set of known BRCA1/2-deficient tumors. The 5th percentile of HRD scores was 42 in the combined breast and ovarian training set, consequently high HRD was defined as HRD scores \( \geq 42 \). The 5th percentile was 41.9 for BRCA1/2-deficient breast tumors and 42.9 for BRCA1/2-deficient ovarian tumors.

HRD scores in the clinical trial cohorts

The PrECOG 0105 patient demographic and clinical data of the patients with evaluable HR status are shown in Supplementary Table S3A. Overall pCR rate in this HR subset of PrECOG 0105 was 23/70 = 33% (31/88 = 35% in the entire study for combined 4 + 6 cycle groups) and the RCB 0/I rate was 40/70 = 57% (51/88 = 58% in the entire study for combined 4 + 6 cycle groups). In the HR-evaluable subset of this cohort, 11 (16%) received 4 cycles of therapy and 59 (84%), 6 cycles. The patient demographic and clinical data of the patients with evaluable HR deficiency is shown for the combined cisplatin trials cohort in Supplementary Table S3B. The frequency of pCR was 18% in the original combined trials (14/79) and 16% in those patients with evaluable HR deficiency status (8/50). The frequency of RCB 0/I was 37% in the original combined trials (29/79) and 34% in those patients with evaluable HR deficiency status (17/50).

The distributions of HRD scores for the two cohorts are shown in Supplementary Fig. S2A and B. The distributions of HRD scores were similar to that seen in the training set, and appear somewhat bimodal in the PrECOG 0105 study and clearly bimodal in the cisplatin trials cohort. Forty-eight of 68 (71%) tumors had a high HRD score (\( \geq 42 \)) in the PrECOG 0105 HRD cohort, whereas in the cisplatin trials HRD cohort, 26 of 48 (54%) had a high HRD.
Association of HR deficiency status with response to platinum-based chemotherapy

HR deficiency was significantly associated with both RCB 0/I and pCR in both the PrECOG 0105 and cisplatin trials cohorts (Table 1). In the PrECOG 0105 cohort, RCB 0/I rates in HR-deficient tumors (n = 50) were 68.0%, compared with 30.0% in HR nondeficient tumors [n = 20; OR = 4.96 (1.61–15.3), P = 0.0036]; pCR rates were 42.0% in HR-deficient and 10.0% in HR nondeficient tumors [OR = 6.52 (1.36–31.2), P = 0.0058]. In the cisplatin trials cohort, RCB 0/I rates in HR-deficient tumors (n = 29) were 51.7%, compared with 9.5% in HR nondeficient tumors [n = 21; OR = 10.18 (2.00–51.89), P = 0.0011]; pCR rates were 27.5% in HR-deficient and 0% in HR nondeficient tumors [OR = 17.00 (1.91–2249), P = 0.0066].

Association of HRD score with response to platinum-based chemotherapy

The distributions of all passing HRD scores by RCB response class for each cohort (N = 68 and N = 48) are shown as box plots in Fig. 2. In the PrECOG 0105 cohort (N = 68), quantitative HRD score (IQR = 28) was significantly associated with RCB 0/I [OR = 2.63 (1.26–5.48), P = 0.0061], but not pCR [OR = 1.85 (0.88–3.88), P = 0.093]. The dichotomous HRD score (high/low) was significantly associated with both RCB 0/I [OR = 4.67 (1.51–14.4), P = 0.0053] and pCR [OR = 6.43 (1.34–30.9), P = 0.0065] in this cohort (Supplementary Table S4A). In the cisplatin trials cohort (N = 48), quantitative HRD was significantly associated with both RCB 0/I [OR = 10.5 (2.3–48.6), P = 3.1 × 10⁻⁴] and pCR [OR = 117 (2.9–4764), P = 7.0 × 10⁻⁵], as was the dichotomous HRD score for RCB 0/I [OR = 10.0 (1.93–51.8), P = 0.0014] and pCR [OR = 17.3 (1.90–2300), P = 0.0071; Supplementary Table S4B]. To assess the performance of the HRD score to place patients into response categories in the combined PrECOG 0105 and cisplatin cohorts, ROC curves of the HRD score predicting RCB 0/I and pCR are shown in Supplementary Fig. S3A and S3B. The AUC values were 0.761 for RCB 0/I and 0.747 for pCR, and the sensitivity at the predefined threshold of 42 is 85% for RCB 0/I and 93% for pCR, consistent with the expectation of 95% sensitivity to detect homologous recombination deficiency.

Table 1. HR deficiency status and association with response to platinum-containing therapy

<table>
<thead>
<tr>
<th>PrECOG 0105 (N = 70)</th>
<th>RCB 0/I = No</th>
<th>RCB 0/I = Yes</th>
<th>pCR = No</th>
<th>pCR = Yes</th>
<th>OR (95% CI)</th>
<th>Reference = Nondeficient</th>
<th>Logistic P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Deficient number (%)</td>
<td>16</td>
<td>34 (68%)</td>
<td>29</td>
<td>21 (42%)</td>
<td>4.96 (1.61–15.3)</td>
<td>6.52 (1.36–31.2)</td>
<td>0.0036</td>
</tr>
<tr>
<td>Nondeficient number (%)</td>
<td>14</td>
<td>6 (30%)</td>
<td>18</td>
<td>2 (10%)</td>
<td>3.65 (1.12–11.6)</td>
<td>0.0058</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Cisplatin Trials Cohort (N = 50)</th>
<th>RCB 0/I = No</th>
<th>RCB 0/I = Yes</th>
<th>pCR = No</th>
<th>pCR = Yes</th>
<th>OR (95% CI)</th>
<th>Reference = Nondeficient</th>
<th>Logistic P</th>
</tr>
</thead>
<tbody>
<tr>
<td>Deficient number (%)</td>
<td>14</td>
<td>15 (51.7%)</td>
<td>21</td>
<td>8 (27.5%)</td>
<td>10.18 (2.00–51.89)</td>
<td>17.00 (1.91–2249)*</td>
<td>0.0066*</td>
</tr>
<tr>
<td>Nondeficient number (%)</td>
<td>19</td>
<td>2 (9.5%)</td>
<td>21</td>
<td>0 (0%)</td>
<td>10.18 (2.00–51.89)</td>
<td>0.0011</td>
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</tbody>
</table>

*Based on Firth’s penalized profile likelihood.
status provided the highest positive predictive value (PPV) of both RCB 0/I and pCR, while its negative predictive value (NPV) is lower compared with HRD score or HR deficiency status; however, these differences were not statistically significant. In the cisplatin trials cohort, BRCA1/2 mutation status, HRD score, and HR deficiency provided similar PPVs for RCB 0/I (43%, 52%, and 52%, respectively) and for pCR (29%, 28%, and 28%, respectively). In this cohort, BRCA1/2 mutation status also gave a lower NPV than either HRD score or HR deficiency status. Younger age at diagnosis was associated with HR deficiency status (\(P = 2.0 \times 10^{-2}\)) and was also associated with improved response (\(P = 0.031\)). However, this association was confounded by BRCA1/2 mutations being more common in younger patients. When mutation status was taken into account, age was no longer a significant predictor of response (\(P = 0.11\)). In univariate analysis of the cisplatin trials cohort (Supplementary Table S5b), only age at diagnosis was associated with HR deficiency status (\(P = 0.037\)). No other clinical variables were associated with either RCB 0/I or HR deficiency status.

### Association of clinical variables with response and HR deficiency status

For the PrECOG 0105 cohort, available clinical variables included clinical stage, tumor grade, age at diagnosis, and number of cycles of chemotherapy; for the cisplatin trials cohort, the clinical variables included use of bevacizumab, tumor size, nodal status, and age at diagnosis. To check for possible confounding, clinical variables were tested first for association with BRCA1/2 mutation status, but were not significant [PrECOG 0105: grade: \(P = 0.38\); stage: \(P = 0.71\) (4 levels; I, II, III, IVA), 0.60 (3 levels; I, II, III)]; chemotherapy cycles: \(P = 0.11\), and age at diagnosis: \(P = 0.12\)]. Cisplatin trials: use of bevacizumab: \(P = 0.73\); nodal status: \(P = 0.23\); tumor size: \(P = 0.90\); age at diagnosis: \(P = 0.53\).

Univariate associations with response and HR deficiency were then tested (Supplementary Table S5). In the PrECOG 0105 cohort (Supplementary Table S5a), tumor grade, stage, and number of cycles of chemotherapy were not statistically significantly associated with RCB 0/I or HR deficiency status. Younger age at diagnosis was associated with HR deficiency status (\(P = 2.0 \times 10^{-2}\)) and was also associated with improved response (\(P = 0.031\)). However, this association was confounded by BRCA1/2 mutations being more common in younger patients. When mutation status was taken into account, age was no longer a significant predictor of response (\(P = 0.11\)). In univariate analysis of the cisplatin trials cohort (Supplementary Table S5b), only age at diagnosis was associated with HR deficiency status (\(P = 0.037\)). No other clinical variables were associated with either RCB 0/I or HR deficiency status.

### HR deficiency status adjusted by clinical covariates

Multivariable logistic regression was used to determine whether HR deficiency status was a significant predictor of RCB 0/I and pCR after adjustment by clinical covariates (Table 3). In the PrECOG 0105 cohort, HR deficiency status (\(P = 0.012\)) and disease stage (\(P = 0.0042\)) were independent predictors of RCB 0/I in multivariable analysis. The interaction between HR deficiency status and stage was not significant when added to the full model (\(P = 0.43\)). In multivariable models of pCR neither HR deficiency status nor clinical variables reached statistical significance (Table 3A). In the cisplatin trials cohort, only HR deficiency status (\(P = 0.0017\)) was a significant predictor of RCB 0/I after adjustment for use of bevacizumab, tumor size, baseline nodal status, and age at diagnosis (Table 3B). In multivariable models of pCR, both HR deficiency (\(P = 0.0063\)) and age at diagnosis (\(P = 0.026\)) were independent predictors of pCR. Interaction between HR deficiency and age was not significant (\(P = 1.0\)).

To estimate the clinical utility of HRD status, logistic regression analysis of 3 models for predicting RCB 0/I and pCR were performed in the combined PrECOG 0105 and cisplatin cohorts (Supplementary Table S6). In each model, cohort was included as a covariate to adjust for possible confounding. The first model included patient stage; the second included stage and tumor BRCA1/2 (tBRCA1/2) mutation status; the third included stage, tBRCA1/2 mutation status, and dichotomous HRD score. For each of these models, a ROC curve was computed (Supplementary Fig. S4A and S4B). For RCB 0/I, the dichotomous HRD score remained significant after adjustment for cohort, clinical stage, and tBRCA1/2 mutation status (\(P = 8.3 \times 10^{-5}\)). AUC was increased from 0.710 to 0.788 by adding dichotomous HRD score to clinical stage and tBRCA1/2 adjusted for cohort (\(P = 0.014\)). For pCR, dichotomous HRD score remained significant.
after adjustment for cohort, clinical stage, and tBRCA1/2 mutation status ($P = 0.0011$). AUC was increased from 0.694 to 0.762 by adding dichotomous HRD score to clinical stage and tBRCA1/2 adjusted for cohort ($P = 0.037$).

### Discussion

In this study, the HRD score (the sum of three metrics of chromosomal level aberration: LOH, TAI, and LST), and the

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**Table 2. BRCA1/2 mutation status (whole cohorts) or HRD score (BRCA1/2 wild-type subset) and associations with response**

**A. BRCA1/2 mutation status**

<table>
<thead>
<tr>
<th>RCB 0/I = no</th>
<th>Mutant number (% response)</th>
<th>Nonmutant number (% response)</th>
<th>OR (95% CI)</th>
<th>Reference = nonmutant</th>
<th>Logistic P</th>
</tr>
</thead>
<tbody>
<tr>
<td>RCB 0/I = no</td>
<td>5 (25%)</td>
<td>24 (27%)</td>
<td>3.27 (1.02-10.5)</td>
<td>0.037</td>
<td></td>
</tr>
<tr>
<td>pCR = no</td>
<td>10 (50%)</td>
<td>35 (29%)</td>
<td>3.18 (1.05-9.63)</td>
<td>0.040</td>
<td></td>
</tr>
<tr>
<td>pCR = yes</td>
<td>10 (24%)</td>
<td>11 (24%)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Cisplatin Trials Cohort (N = 45)**

<table>
<thead>
<tr>
<th>RCB 0/I = no</th>
<th>Mutant number (% response)</th>
<th>Nonmutant number (% response)</th>
<th>OR (95% CI)</th>
<th>Reference = nonmutant</th>
<th>Logistic P</th>
</tr>
</thead>
<tbody>
<tr>
<td>RCB 0/I = no</td>
<td>4 (40%)</td>
<td>26 (39%)</td>
<td>1.62 (0.31-8.43)</td>
<td>0.57</td>
<td></td>
</tr>
<tr>
<td>pCR = no</td>
<td>5 (50%)</td>
<td>33 (40%)</td>
<td>2.64 (0.40-17.5)</td>
<td>0.33</td>
<td></td>
</tr>
<tr>
<td>pCR = yes</td>
<td>2 (28%)</td>
<td>5 (33%)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**B. HRD Score ≥42 (high vs. low), subset of BRCA1/2 wild-type tumors**

<table>
<thead>
<tr>
<th>RCB 0/I = no</th>
<th>HRD high number (% response)</th>
<th>HRD low number (% response)</th>
<th>OR (95% CI)</th>
<th>Reference = low HRD score</th>
<th>Logistic P</th>
</tr>
</thead>
<tbody>
<tr>
<td>RCB 0/I = no</td>
<td>11 (22.4%)</td>
<td>13 (20.3%)</td>
<td>3.15 (0.92-10.8)</td>
<td>0.062</td>
<td></td>
</tr>
<tr>
<td>pCR = no</td>
<td>16 (39%)</td>
<td>6 (32%)</td>
<td>4.25 (0.80-22.6)</td>
<td>0.063</td>
<td></td>
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<tr>
<td>pCR = yes</td>
<td>9 (33%)</td>
<td>2 (11%)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Cisplatin Trials Cohort (N = 38)**

<table>
<thead>
<tr>
<th>RCB 0/I = no</th>
<th>HRD high number (% response)</th>
<th>HRD low number (% response)</th>
<th>OR (95% CI)</th>
<th>Reference = low HRD score</th>
<th>Logistic P</th>
</tr>
</thead>
<tbody>
<tr>
<td>RCB 0/I = no</td>
<td>9 (23.7%)</td>
<td>17 (25.5%)</td>
<td>9.44 (1.69-52.7)</td>
<td>0.0039</td>
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<tr>
<td>pCR = no</td>
<td>14 (52.6%)</td>
<td>2 (10.5%)</td>
<td>14.79 (1.49-201)</td>
<td>0.018</td>
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<tr>
<td>pCR = yes</td>
<td>5 (26.3%)</td>
<td>0 (0%)</td>
<td></td>
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</tbody>
</table>

**Figure 3.**

Relative response rates for PrECOG 0105 (A) and in the cisplatin cohort (B) stratified by HRD score, BRCA1/2 mutation status, and HR deficiency status. WT, wild-type, M, mutant.

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null
experiences using cytotoxic chemotherapies suggests that HR deficiency may also predict responses to topoisomerase inhibitors such as the anthracyclines and alkylating agents (30, 31). This study and others suggest that HR deficiency may identify the patients who would benefit from treatment with DNA-damaging agents such as platinum.

In summary, in this analysis, HRD status provides significant improvement over clinical variables or BRCA1/2 mutation status in identifying tumors with an increased likelihood of response to platinum-based neoadjuvant therapy among patients with TNBC. Clinical use of the HRD test has the potential to identify sporadic TNBC patients likely to respond to DNA-damaging therapy beyond those currently identified by germline BRCA1/2 mutation screening. The clinical trials described here do not include a nonplatinum comparator arm. Additional studies, including retrospective analysis of larger clinical trials with a control arm or prospective clinical trials, will further define and clarify the clinical utility of the HR deficiency assay and ultimately determine the range of chemotherapies for which HR deficiency may predict response.

Disclosure of Potential Conflicts of Interest

G.B. Mills has ownership interest (including patents) in Catena Pharmaceuticals, PTV Ventures, SpindleTop Ventures, and Myriad Genetics, reports receiving speakers bureau honoraria from AstraZeneca, Eli Lilly, ISIS Pharmaceuticals, Nuevolution, and Symphogen, is a consultant/advisory board member for Adventist Health, AstraZeneca, Blend, Catena Pharmaceuticals, Critical Outcome Technologies, Halal Bio Korea, ImmunoMET, Millennium Pharmaceuticals, Nuevolution, Precision Medicine, Provista Diagnostics, Signalkem Life- sciences, and Symphogen, and reports receiving commercial research grants from Adelson Medical Research Foundation, AstraZeneca, Critical Outcome Technologies, Komen Research Foundation, and Nanostrong. S.J. Isakoff is a consultant/advisory board member for Myriad Genetics. K.M. Timms, A. Gutin, and V. Abkevich have ownership interest (including patents) in Myriad Genetics. J.E. Garber reports receiving commercial research grants from Amgen Genetics and Myriad Genetics. J.M. Ford reports receiving commercial research grants from Myriad Genetics and Natera. D.P. Silver and A.L. Richardson are listed as co-inventors on a patent on telomeric allelic imbalance, which is owned by the Dana-Farber Cancer Institute and licensed to Myriad Genetics. No potential conflicts of interest were disclosed by the other authors.

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